

RESPONSE

I. Restriction Requirement

The Examiner has determined that the original claims are directed to six separate and distinct inventions under 35 U.S.C. § 121, as follows:

- Group I: Claims 1, drawn to an isolated nucleic molecule, classified in 536 subclass 23.1.
- Group II: Claim 2, drawn to an isolated nucleic molecule, classified in 536 subclass 23.1.
- Group III: Claim 3, drawn to an isolated nucleic molecule, classified in 536 subclass 23.1.
- Group IV: Claim 4, drawn to an isolated nucleic molecule, classified in 536 subclass 23.1.
- Group V: Claim 5, drawn to an isolated nucleic molecule, classified in 536 subclass 23.1.
- Group VI: Claim 6, drawn to an isolated nucleic molecule, classified in 536 subclass 23.1.

II. Response to Restriction Requirement

In response to the Restriction Requirement mailed September 24, 2003 (Paper No. 6), Applicants respectfully request reconsideration of this requirement based on the fact that the amino acid sequences described in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6 and SEQ ID NO: 8 are all encoded by a common genetic locus and are therefore not independent.

However, first it should be noted that claims 1, 2 and 3 clearly refer to the same invention, as the nucleic acid of Claim 1 (SEQ ID NO:1) meets all of the criteria of Claims 2 (encodes the amino acid of SEQ ID NO:2 and would hybridize to itself) and Claim 3 (encodes the amino acid of SEQ ID NO:2). Therefore, clearly, Groups I (Claim 1), II (Claim 2) and III (Claim 3) represent a single invention.

Furthermore, Applicants invite the Examiner's attention to Exhibit A which contains the results of an amino acid comparison between SEQ ID NO:2 and SEQ ID NO:8, SEQ ID NO:6 or SEQ ID NO:4 of the present invention. From this comparison it can be seen that SEQ ID NO:2 and SEQ ID NO:8 differ by a single amino acid in 4589 amino acids (99.978% identity). Likewise, SEQ ID NO:6 is identical over its entire sequence to SEQ ID NO:2, except for the first 4 amino acids. Similarly, SEQ ID NO:4 is merely a slightly shorter variant of SEQ ID NO: 2 that results from the use of an earlier stop codon (the first 3852 amino acids of the 4585 amino acids of SEQ ID NO:2). Therefore, clearly SEQ ID NO: 2, SEQ ID NO: 8, SEQ ID NO:6 and SEQ ID NO:4 represent variants of the same gene.

In the alternative, Applicants provisionally elect with traverse to prosecute the claims of Groups I/II/III which are more properly combined into a single group (as SEQ ID NO:1 encodes SEQ ID NO:2, see above). Applicants further elect, pursuant to 35 U.S.C. § 121, the species of SEQ ID NO: 1 (and the amino acid sequence it encodes, SEQ ID NO:2 for initial examination on the merits. Elected claims 1, 2 and 3 read on the elected species. Applicants understand their species election is being made solely to expedite examination of the application, and that they are entitled to consideration of additional species upon allowance of a generic claim. Applicants reserve the right to refile claims to the non-elected inventions in one or more future applications retaining the priority date of the present case and the earlier cited priority applications.

III. Status of the Claims

Claim 1 has been amended to further clarify the claim.. Claims 1-5 are therefore pending.

IV. Support for the Claims

Claim 1 has been amended to further clarify the claim. Support for this claim can be found throughout the specification as originally filed, with particular support being found at least in original Claim 1 and the Sequence Listing as originally filed. As amended Claim 1 is fully supported by the specification and claim as originally filed, does not constitute new matter.

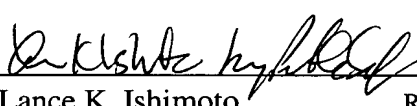
V. Conclusion

The present document is a complete response to the Restriction and Species Election Requirement. Applicants believe that the claims of the instant application meet all of the conditions for

patentability and are in condition for allowance. Accordingly, an early indication of the same is respectfully requested. Should Examiner Teller have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

October 23, 2003
Date


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Customer # 24231

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAlmaGuc: 4589 aa

LEX 285 SEQ ID NO:2

vs. /tmp/fastaDAAlmaGuc library

searching /tmp/fastaDAAlmaGuc library

4588 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 51, opt: 39, gap-pen: -12/ -2, width: 16
Scan time: 0.200

The best scores are:

opt

LEX 285 SEQ ID NO:8

(4588) 30025

>>LEX 285 SEQ ID NO:8

(4588 aa)

initn: 26943 init1: 26943 opt: 30025

Smith-Waterman score: 30025; 99.978% identity in 4589 aa overlap (1-4589:1-4588)

	10	20	30	40	50	60
LEX	MDIIMGHCVGTRPPACCLILLLFKLLATVSQGLPGTGPLGFHFTHSIYNATVYENSAART					
					
LEX	MDIIMGHCVGTRPPACCLILLLFKLLATVSQGLPGTGPLGFHFTHSIYNATVYENSAART					
	10	20	30	40	50	60
	70	80	90	100	110	120
LEX	YVNSQSRMGITLIDLSWDIKYRIVSGDEEGFFKAEVVIADFCFLRIRTKGGNSAILNRE					
					
LEX	YVNSQSRMGITLIDLSWDIKYRIVSGDEEGFFKAEVVIADFCFLRIRTKGGNSAILNRE					
	70	80	90	100	110	120
	130	140	150	160	170	180
LEX	IQDNYLLIVKGSVRGEDLEAWTKVNIQVLDMNDLRPLFSPTTYSVTIAESTPLRTSVAQV					
					
LEX	IQDNYLLIVKGSVRGEDLEAWTKVNIQVLDMNDLRPLFSPTTYSVTIAESTPLRTSVAQV					
	130	140	150	160	170	180
	190	200	210	220	230	240
LEX	TATDADIGSNGEFYYYFKNKVDLFSVHPTSGVISLSGRLNYDEKNRYDLEILAVDRGMKL					
					
LEX	TATDADIGSNGEFYYYFKNKVDLFSVHPTSGVISLSGRLNYDEKNRYDLEILAVDRGMKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
LEX	YGNGVSSSTAKLYVHIERINEHAPTIVVTHVPFSLKEPTYAVVTVDLDDGANGEIES					
					
LEX	YGNGVSSSTAKLYVHIERINEHAPTIVVTHVPFSLKEPTYAVVTVDLDDGANGEIES					
	250	260	270	280	290	300
	310	320	330	340	350	360
LEX	VSIVAGDPLDQFFLAKEGKWLNEYKIKERKQIDWESFPYGYNLTLQAKDKGSPQKCSALK					
					
LEX	VSIVAGDPLDQFFLAKEGKWLNEYKIKERKQIDWESFPYGYNLTLQAKDKGSPQKCSALK					
	310	320	330	340	350	360

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      370      380      390      400      410      420
LEX  AVYIGNPTRDTPVPIRFEKEVYDVSISEFSPPGVVVAIVKLSPEPIDVEYKLSPGEDAVYF
      .....
LEX  AVYIGNPTRDTPVPIRFEKEVYDVSISEFSPPGVVVAIVKLSPEPIDVEYKLSPGEDAVYF
      370      380      390      400      410      420

      430      440      450      460      470      480
LEX  KINPRSGLIVTARPLNTVKKEVYKLEVTNKEGDLKAQVTISIEDANDHTPEFQQPLYDAY
      .....
LEX  KINPRSGLIVTARPLNTVKKEVYKLEVTNKEGDLKAQVTISIEDANDHTPEFQQPLYDAY
      430      440      450      460      470      480

      490      500      510      520      530      540
LEX  VNESVPVGTSVLTVSASDKDKGENGYITYSIASLNLFPVINQFTGVISTTEELDFESSP
      .....
LEX  VNESVPVGTSVLTVSASDKDKGENGYITYSIASLNLFPVINQFTGVISTTEELDFESSP
      490      500      510      520      530      540

      550      560      570      580      590      600
LEX  EIYRFIVRASDWGSPYRHESEVNVNVTIRIGNVNDNSPLFEKVACQGVISYDFPVGGHITAV
      .....
LEX  EIYRFIVRASDWGSPYRHESEVNVNVTIRIGNVNDNSPLFEKVACQGVISYDFPVGGHITAV
      550      560      570      580      590      600

      610      620      630      640      650      660
LEX  SAIDIDELELVKYKIIISGNELGFFYLNPD SGVLQLKKSLTNSGIKNGNFALRITATDGEN
      .....
LEX  SAIDIDELELVKYKIIISGNELGFFYLNPD SGVLQLKKSLTNSGIKNGNFALRITATDGEN
      610      620      630      640      650      660

      670      680      690      700      710      720
LEX  LADPMSINISVLHGKVSSKSFSCRETRVAQKLAEKLLIKAKANGKLNLEDGFLDFYSINR
      .....
LEX  LADPMSINISVLHGKVSSKSFSCRETRVAQKLAEKLLIKAKANGKLNLEDGFLDFYSINR
      670      680      690      700      710      720

      730      740      750      760      770      780
LEX  QGPYFDKSFPSDVAVKEDLPVGANILKIKAYDADSGFNGKVLFTISDGNTDSCFNIDMET
      .....
LEX  QGPYFDKSFPSDVAVKEDLPVGANILKIKAYDADSGFNGKVLFTISDGNTDSCFNIDMET
      730      740      750      760      770      780

      790      800      810      820      830      840
LEX  GQLKVLMPMDREHTDLYLLNITIYDLGNPQKSSWRLLTINVEDANDNSPVFIQDSYSVNI
      .....
LEX  GQLKVLMPMDREHTDLYLLNITIYDLGNPQKSSWRLLTINVEDANDNSPVFIQDSYSVNI
      790      800      810      820      830      840

      850      860      870      880      890      900
LEX  LESSGIGTEIIQVEARDKDLGSNGEVTYSVLTDTQQFAINSSTGIVYVADQLDRESKANY
      .....
LEX  LESSGIGTEIIQVEARDKDLGSNGEVTYSVLTDTQQFAINSSTGIVYVADQLDRESKANY
      850      860      870      880      890      900

      910      920      930      940      950      960
LEX  SLKIEARDKAESGQQLFSVVTLKVFLDDVND CSPAFIPSSYSVKVLEDLPVGTVIAWLET
      .....
LEX  SLKIEARDKAESGQQLFSVVTLKVFLDDVND CSPAFIPSSYSVKVLEDLPVGTVIAWLET
      910      920      930      940      950      960
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          970      980      990      1000      1010      1020
LEX   HDPDLGLGGQVRYSLVNDYNGRFEIDKASGAIRLSKELDYEQQFYNLTVRAKDKGRPVS
      .....
LEX   HDPDLGLGGQVRYSLVNDYNGRFEIDKASGAIRLSKELDYEQQFYNLTVRAKDKGRPVS
          970      980      990      1000      1010      1020

          1030      1040      1050      1060      1070      1080
LEX   LSSVSFVEVEVVDVNNENLHTPYFPDFAVVGSVKENSRIGTSVLQVTARDEDSGRDGEIQY
      .....
LEX   LSSVSFVEVEVVDVNNENLHTPYFPDFAVVGSVKENSRIGTSVLQVTARDEDSGRDGEIQY
          1030      1040      1050      1060      1070      1080

          1090      1100      1110      1120      1130      1140
LEX   SIRDGSGLGGRFSIDDESGVITAADILDRETMGSYWLTVYATDRGVVPLYSTIEVYIEVED
      .....
LEX   SIRDGSGLGGRFSIDDESGVITAADILDRETMGSYWLTVYATDRGVVPLYSTIEVYIEVED
          1090      1100      1110      1120      1130      1140

          1150      1160      1170      1180      1190      1200
LEX   VNDNAPLTSEPIIYYPVVMENSPKDVSVIQUIQAEDPDSSSNEKLTYRITSGNPQNFFAINI
      .....
LEX   VNDNAPLTSEPIIYYPVVMENSPKDVSVIQUIQAEDPDSSSNEKLTYRITSGNPQNFFAINI
          1150      1160      1170      1180      1190      1200

          1210      1220      1230      1240      1250      1260
LEX   KTGLITTTSRKLDREQQAEHFLEVTVTDGGPSPKQSTIWVVVQVLDENDNKPQFPEKVYQ
      .....
LEX   KTGLITTTSRKLDREQQAEHFLEVTVTDGGPSPKQSTIWVVVQVLDENDNKPQFPEKVYQ
          1210      1220      1230      1240      1250      1260

          1270      1280      1290      1300      1310      1320
LEX   IKLPERDRKKRGEPIYRAFAFDRDEGPNAEISYSIVDGNDDGKFFIDPKTGMVSSRKQFT
      .....
LEX   IKLPERDRKKRGEPIYRAFAFDRDEGPNAEISYSIVDGNDDGKFFIDPKTGMVSSRKQFT
          1270      1280      1290      1300      1310      1320

          1330      1340      1350      1360      1370      1380
LEX   AGSYDILTIKAVDNGRPPQKSSTARLHIEWIKKPPPSPIPLTFDEPFYNFTVMESDRVTEI
      .....
LEX   AGSYDILTIKAVDNGRPPQKSSTARLHIEWIKKPPPSPIPLTFDEPFYNFTVMESDRVTEI
          1330      1340      1350      1360      1370      1380

          1390      1400      1410      1420      1430      1440
LEX   VGVVSVQPANTPLWFDIVGGNFDSAFDAEKGVTIVIAKPLDAEQRSIYNMSVEVTDGTN
      .....
LEX   VGVVSVQPANTPLWFDIVGGNFDSAFDAEKGVTIVIAKPLDAEQRSIYNMSVEVTDGTN
          1390      1400      1410      1420      1430      1440

          1450      1460      1470      1480      1490      1500
LEX   VAVTQVFIKVLNNDNGPEFSQPNYDVTISEDVLPDTEILQIEATDRDEKHKLSYTVHSS
      .....
LEX   VAVTQVFIKVLNNDNGPEFSQPNYDVTISEDVLPDTEILQIEATDRDEKHKLSYTVHSS
          1450      1460      1470      1480      1490      1500

          1510      1520      1530      1540      1550      1560
LEX   IDSISMRKFRIDPSTGVLYTAERLDHEAQDKHILNIMVRDQEFPYRRNLARVIVNVEDAN
      .....
LEX   IDSISMRKFRIDPSTGVLYTAERLDHEAQDKHILNIMVRDQEFPYRRNLARVIVNVEDAN
          1510      1520      1530      1540      1550      1560
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1570      1580      1590      1600      1610      1620
LEX DHSPYFTNPLYEASVFESAAALGSAVLQVTALDKDKGENAELIYTIEAGNTGTMFKIEPVL
LEX DHSPYFTNPLYEASVFESAAALGSAVLQVTALDKDKGENAELIYTIEAGNTGTMFKIEPVL
1570      1580      1590      1600      1610      1620

1630      1640      1650      1660      1670      1680
LEX GIITICKEPDMTTMGQFVLSIKVTDQGSPPMSATAIVRISVTMSDNSHPKFIHKDYQAEV
LEX GIITICKEPDMTTMGQFVLSIKVTDQGSPPMSATAIVRISVTMSDNSHPKFIHKDYQAEV
1630      1640      1650      1660      1670      1680

1690      1700      1710      1720      1730      1740
LEX NENVDIGTSVILISAIQSSTLIYEVKDG DINGIFTINPYSGVITTQKALDYERTSSYQLI
LEX NENVDIGTSVILISAIQSSTLIYEVKDG DINGIFTINPYSGVITTQKALDYERTSSYQLI
1690      1700      1710      1720      1730      1740

1750      1760      1770      1780      1790      1800
LEX IQATNMAGMASNATVNIQIVDENDNAPVFLFSQYSGSLSEAAPINSIVRSLDNSPLVIRA
LEX IQATNMAGMASNATVNIQIVDENDNAPVFLFSQYSGSLSEAAPINSIVRSLDNSPLVIRA
1750      1760      1770      1780      1790      1800

1810      1820      1830      1840      1850      1860
LEX TDADSNRNALLVYQIVESTAKKFFTVD SSTGAIRTIANLDHETIAHFHFHVHVRDSGSPQ
LEX TDADSNRNALLVYQIVESTAKKFFTVD SSTGAIRTIANLDHETIAHFHFHVHVRDSGSPQ
1810      1820      1830      1840      1850      1860

1870      1880      1890      1900      1910      1920
LEX LTAESPVEVNIEVTDVNDNPPVFTQAVFETILLPT YVGVEVLKVSATDPDSEVPPELTY
LEX LTAESPVEVNIEVTDVNDNPPVFTQAVFETILLPT YVGVEVLKVSATDPDSEVPPELTY
1870      1880      1890      1900      1910      1920

1930      1940      1950      1960      1970      1980
LEX SLMEGSLDHFLIDSNSGVLTIKNNNLSKDH YMLIVKVSDGKFYSTSMVTIMVKEAMDSGL
LEX SLMEGSLDHFLIDSNSGVLTIKNNNLSKDH YMLIVKVSDGKFYSTSMVTIMVKEAMDSGL
1930      1940      1950      1960      1970      1980

1990      2000      2010      2020      2030      2040
LEX HFTQSFYSTSISENNITNITKVAIVNAVGNRLNE PLKYSILNPGNKFKIKSTSGVIQTTGV
LEX HFTQSFYSTSISENNITNITKVAIVNAVGNRLNE PLKYSILNPGNKFKIKSTSGVIQTTGV
1990      2000      2010      2020      2030      2040

2050      2060      2070      2080      2090      2100
LEX PFDREEQELYELVVEASRELDHLRVARVVVRV NIEDINDNSPVFVGLPYAAVQVDAEPG
LEX PFDREEQELYELVVEASRELDHLRVARVVVRV NIEDINDNSPVFVGLPYAAVQVDAEPG
2050      2060      2070      2080      2090      2100

2110      2120      2130      2140      2150      2160
LEX TLIYQVTAIDKDKGPNGEVTYVLQDDYGHFEI NPNSGNVILKEAFNSDLSNIEYGVVTLA
LEX TLIYQVTAIDKDKGPNGEVTYVLQDDYGHFEI NPNSGNVILKEAFNSDLSNIEYGVVTLA
2110      2120      2130      2140      2150      2160
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10/21/2003

10/21/2003

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      3370      3380      3390      3400      3410      3420
LEX  ILLIAEDVDSQPNGQIHFSIVNGDRDNEFTVDPVLGLVKVKKKLDREVRSGYSLLVQAVD
      .....
LEX  ILLIAEDVDSQPNGQIHFSIVNGDRDNEFTVDPVLGLVKVKKKLDREVRSGYSLLVQAVD
      3370      3380      3390      3400      3410      3420

      3430      3440      3450      3460      3470      3480
LEX  SGIPAMSSTATVNIDISDVNDNSPVFTFANYTAVIQENKPVGTSILQLVVTDRDSFHNGP
      .....
LEX  SGIPAMSSTATVNIDISDVNDNSPVFTFANYTAVIQENKPVGTSILQLVVTDRDSFHNGP
      3430      3440      3450      3460      3470      3480

      3490      3500      3510      3520      3530      3540
LEX  PFSFSILSGNEEEFVLDPHGILRSVAVFQHTESLEYVLCVQAKDSGKPPQVSHTYIRVR
      .....
LEX  PFSFSILSGNEEEFVLDPHGILRSVAVFQHTESLEYVLCVQAKDSGKPPQVSHTYIRVR
      3490      3500      3510      3520      3530      3540

      3550      3560      3570      3580      3590      3600
LEX  VIEESTHKPTAIPLEIFIVTMEDDFPGGVIGKIHATDQDMYDVLTFALKSEQKSLFKVNS
      .....
LEX  VIEESTHKPTAIPLEIFIVTMEDDFPGGVIGKIHATDQDMYDVLTFALKSEQKSLFKVNS
      3550      3560      3570      3580      3590      3600

      3610      3620      3630      3640      3650      3660
LEX  HDGKIIALGGLDSGKYVLNVSVSDGRFQVPIDVVHVEQLVHEMLQNTVTIRFENVSPED
      .....
LEX  HDGKIIALGGLDSGKYVLNVSVSDGRFQVPIDVVHVEQLVHEMLQNTVTIRFENVSPED
      3610      3620      3630      3640      3650      3660

      3670      3680      3690      3700      3710      3720
LEX  FVGLHMHGFRRTLRLNAVLTQKQDSLRIISIQPVAGTNQLDMLFAVEMHSSEFYKPAYLIQ
      .....
LEX  FVGLHMHGFRRTLRLNAVLTQKQDSLRIISIQPVAGTNQLDMLFAVEMHSSEFYKPAYLIQ
      3670      3680      3690      3700      3710      3720

      3730      3740      3750      3760      3770      3780
LEX  KLSNARRHLENIMRISAILEKNCSGLDCQEQHCEQGLSLDSHALMTYSTARISFVCPRFY
      .....
LEX  KLSNARRHLENIMRISAILEKNCSGLDCQEQHCEQGLSLDSHALMTYSTARISFVCPRFY
      3730      3740      3750      3760      3770      3780

      3790      3800      3810      3820      3830      3840
LEX  RNVRCCTCNGGLCPGSNDPCVEKPCPGDMQCVGYEASRRPFLCQCPPGKLGECSGHTSLSF
      .....
LEX  RNVRCCTCNGGLCPGSNDPCVEKPCPGDMQCVGYEASRRPFLCQCPPGKLGECSGHTSLSF
      3790      3800      3810      3820      3830      3840

      3850      3860      3870      3880      3890      3900
LEX  AGNSYIKYRLSENSKEEDFKLALRLRTLQSNGIIMYTRANPCIILKIVDGKLWFQLDCGS
      .....
LEX  AGNSYIKYRLSENSKEEDFKLALRLRTLQSNGIIMYTRANPCIILKIVDGKLWFQLDCGS
      3850      3860      3870      3880      3890      3900

      3910      3920      3930      3940      3950      3960
LEX  GPGILGISGRAVNDGSWHSVFLELNRNFTSLSLDDSYVERRRAPLYFQTLSTESSIYFGA
      .....
LEX  GPGILGISGRAVNDGSWHSVFLELNRNFTSLSLDDSYVERRRAPLYFQTLSTESSIYFGA
      3910      3920      3930      3940      3950      3960
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          3970      3980      3990      4000      4010      4020
LEX  LVQADNIRSLTDRVTQVLSGFQGC LDSVILNNNELPLQNKRSSFAEVVGLTELKLGCVL
LEX  LVQADNIRSLTDRVTQVLSGFQGC LDSVILNNNELPLQNKRSSFAEVVGLTELKLGCVL
          3970      3980      3990      4000      4010      4020

          4030      4040      4050      4060      4070      4080
LEX  YPDACKRSPCQHGGSC TGLPSGGYQCTCLSQFTGRNCESEITACFPNPCRNGGSCDPIGN
LEX  YPDACKRSPCQHGGSC TGLPSGGYQCTCLSQFTGRNCESEITACFPNPCRNGGSCDPIGN
          4030      4040      4050      4060      4070      4080

          4090      4100      4110      4120      4130      4140
LEX  TFICNCKAGLTGVTCEEDINECERECEENG GSCVNVFGSFLCNCTPGYVGQYCGLRPVVV
LEX  TFICNCKAGLTGVTCEEDINECERECEENG GSCVNVFGSFLCNCTPGYVGQYCGLRPVVV
          4090      4100      4110      4120      4130

          4150      4160      4170      4180      4190      4200
LEX  PNIQAGHSYVGKEELIGIAVVL FVIFILVVL FIVFRKKVFRKNYSRNNITLVQDPATAAL
LEX  PNIQAGHSYVGKEELIGIAVVL FVIFILVVL FIVFRKKVFRKNYSRNNITLVQDPATAAL
4140      4150      4160      4170      4180      4190

          4210      4220      4230      4240      4250      4260
LEX  LNKSNIGIPFRNLRGSGDGRNVYQEVGPPQVPVRPMAYTPCFQSDSRSNLDKIVDGLGGEH
LEX  LNKSNIGIPFRNLRGSGDGRNVYQEVGPPQVPVRPMAYTPCFQSDSRSNLDKIVDGLGGEH
4200      4210      4220      4230      4240      4250

          4270      4280      4290      4300      4310      4320
LEX  QEMTTFHPESPRI LTARRGVVVC SVAPNLPAVSPCRSDCDSIRKNGWDAGTENKGVDDPG
LEX  QEMTTFHPESPRI LTARRGVVVC SVAPNLPAVSPCRSDCDSIRKNGWDAGTENKGVDDPG
4260      4270      4280      4290      4300      4310

          4330      4340      4350      4360      4370      4380
LEX  EVTCFAGSNKGSNSEVQSLSSFQSDSGDDNASIVTVIQLVNNVVD TIENEVSVM DQGQNY
LEX  EVTCFAGSNKGSNSEVQSLSSFQSDSGDDNASIVTVIQLVNNVVD TIENEVSVM DQGQNY
4320      4330      4340      4350      4360      4370

          4390      4400      4410      4420      4430      4440
LEX  NRAYHWDTS DWM PGARLS D IEEV PNYENQDGGSAHQGSTRELES DYYLGGYDIDSEYPPP
LEX  NRAYHWDTS DWM PGARLS D IEEV PNYENQDGGSAHQGSTRELES DYYLGGYDIDSEYPPP
4380      4390      4400      4410      4420      4430

          4450      4460      4470      4480      4490      4500
LEX  HEEEFLSQDQLPPPLPEDFPDQYEALPPSQPVSLASTLS PDCRRRPQFHPSQYLP PPHFPF
LEX  HEEEFLSQDQLPPPLPEDFPDQYEALPPSQPVSLASTLS PDCRRRPQFHPSQYLP PPHFPF
4440      4450      4460      4470      4480      4490

          4510      4520      4530      4540      4550      4560
LEX  NETDLVGPPASCE FSTFAVSMNQGT EPTGPADSVSLSLHNSRG TSSSDVSANCGFDDSEV
LEX  NETDLVGPPASCE FSTFAVSMNQGT EPTGPADSVSLSLHNSRG TSSSDVSANCGFDDSEV
4500      4510      4520      4530      4540      4550
```

Function used was FASTA

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAp9aw9W: 4589 aa

>LEX 285 SEQ ID NO:2

vs /tmp/fastaDAAq9aw9W library

searching /tmp/fastaDAAq9aw9W library

4585 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2

join: 51, opt: 39, gap-pen: -12/ -2, width: 16

Scan time: 0.200

The best scores are:

opt

LEX 285 SEQ ID NO:6

(4585) 30017

>>LEX 285 SEQ ID NO:6

(4585 aa)

initn: 30017 initl: 30017 opt: 30017

Smith-Waterman score: 30017; 100.000% identity in 4585 aa overlap (5-4589:1-4585)

	10	20	30	40	50	60
LEX	MDIIMGHCVGTRPPACCLILLLFKLLATVSQGLPGTGPLGFHFTHSIYNATVYENSAART					
LEX	MGHCVGTRPPACCLILLLFKLLATVSQGLPGTGPLGFHFTHSIYNATVYENSAART					
	10	20	30	40	50	
	70	80	90	100	110	120
LEX	YVNSQSRMGITLIDLSDWKYRIVSGDEEGFFKAEEVIIADFCFLRIRTKGGNSAILNRE					
LEX	YVNSQSRMGITLIDLSDWKYRIVSGDEEGFFKAEEVIIADFCFLRIRTKGGNSAILNRE					
	60	70	80	90	100	110
	130	140	150	160	170	180
LEX	IQDNYLLIVKGSVRGEDLEAWTKVNIQVLDMDNLRPLFSPTTYSVTIAESTPLRTSVAQV					
LEX	IQDNYLLIVKGSVRGEDLEAWTKVNIQVLDMDNLRPLFSPTTYSVTIAESTPLRTSVAQV					
	120	130	140	150	160	170
	190	200	210	220	230	240
LEX	TATDADIGSNGEFYYYFKNKVDLFSVHPTSGVISLSGRLNYDEKNRYDLEILAVDRGMKL					
LEX	TATDADIGSNGEFYYYFKNKVDLFSVHPTSGVISLSGRLNYDEKNRYDLEILAVDRGMKL					
	180	190	200	210	220	230
	250	260	270	280	290	300
LEX	YGNNGVSSTAKLYVHIERINEHAPTIHVVTHVPFSLEKEPTYAVVTVDLDDGANGEIES					
LEX	YGNNGVSSTAKLYVHIERINEHAPTIHVVTHVPFSLEKEPTYAVVTVDLDDGANGEIES					
	240	250	260	270	280	290
	310	320	330	340	350	360
LEX	VSIVAGDPLDQFFLAKEGKWLNEYKIKERKQIDWESFPYGYNLTQAKDKGSPQKCSALK					
LEX	VSIVAGDPLDQFFLAKEGKWLNEYKIKERKQIDWESFPYGYNLTQAKDKGSPQKCSALK					
	300	310	320	330	340	350

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      370      380      390      400      410      420
LEX  AVYIGNPTRDTPVIRFEKEVYDVSISEFSPPGVVVAIVKLSPEPIDVEYKLSPGEDAVYF
LEX  .....
      360      370      380      390      400      410

      430      440      450      460      470      480
LEX  KINPRSGLIVTARPLNTVKKEVYKLEVTNKEGDLKAQVTISIEDANDHTPEFQQPLYDAY
LEX  .....
      420      430      440      450      460      470

      490      500      510      520      530      540
LEX  VNESVPVGTSVLTVSASDKDKGENGYITYSIASLNLLPFVINQFTGVISTTEELDFESSP
LEX  .....
      480      490      500      510      520      530

      550      560      570      580      590      600
LEX  EIYRFIVRASDWGSPYRHESEVNVITIRIGNVNDNSPLFEKVACQGVISYDFPVGGHITAV
LEX  .....
      540      550      560      570      580      590

      610      620      630      640      650      660
LEX  SAIDIDELELVKYKIISGNELGFFYLNPD SGVLQLKKSLTNSGIKNGNFALRITATDGEN
LEX  .....
      600      610      620      630      640      650

      670      680      690      700      710      720
LEX  LADPMSINISVLHGKVSSKSFSCRETRVAQKLAEKLLIKAKANGKLNLEDGFLDFYSINR
LEX  .....
      660      670      680      690      700      710

      730      740      750      760      770      780
LEX  QGPYFDKSFPSDVAVKEDLPVGANILKIKAYDADSGFNGKVLFTISDGNTDSCFNIDMET
LEX  .....
      720      730      740      750      760      770

      790      800      810      820      830      840
LEX  GQLKVLMPMDREHTDLYLLNITIYDLGNPQKSSWRLLTINVEDANDNSPVFIQDSYSVNI
LEX  .....
      780      790      800      810      820      830

      850      860      870      880      890      900
LEX  LESSGIGTEIIQVEARDKDLGSNGEVTVSVLTD TQQFAINSSTGIVYVADQLDRESKANY
LEX  .....
      840      850      860      870      880      890

      910      920      930      940      950      960
LEX  SLKIEARDKAESGQQLFSVVT LKVFLLDDVND CSPAFIPSSYSVKVLEDLPVGTVIAWLET
LEX  .....
      900      910      920      930      940      950
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          970      980      990      1000      1010      1020
LEX  HDPDLGLGGQVRYSLVNDYNGRFEIDKASGAIRLSKELDYEQQFYNLTVRAKDKGRPV
LEX  HDPDLGLGGQVRYSLVNDYNGRFEIDKASGAIRLSKELDYEQQFYNLTVRAKDKGRPV
          960      970      980      990      1000      1010

          1030      1040      1050      1060      1070      1080
LEX  LSSVSFVEVEVVDVNNENLHTPYFPDFAVVGSVKENSRIGTSVLQVTARDEDSGRDGEIQ
LEX  LSSVSFVEVEVVDVNNENLHTPYFPDFAVVGSVKENSRIGTSVLQVTARDEDSGRDGEIQ
          1020      1030      1040      1050      1060      1070

          1090      1100      1110      1120      1130      1140
LEX  SIRDGSGGLGRFSIDDESGVITAADILDRETMGSYWLTVYATDRGVVPLYSTIEVYIEVED
LEX  SIRDGSGGLGRFSIDDESGVITAADILDRETMGSYWLTVYATDRGVVPLYSTIEVYIEVED
          1080      1090      1100      1110      1120      1130

          1150      1160      1170      1180      1190      1200
LEX  VNDNAPLTSEPIIYPVVMENSPKDVSVIQUIAEDPDSSSNEKLTYRITSGNPQNFFAINI
LEX  VNDNAPLTSEPIIYPVVMENSPKDVSVIQUIAEDPDSSSNEKLTYRITSGNPQNFFAINI
          1140      1150      1160      1170      1180      1190

          1210      1220      1230      1240      1250      1260
LEX  KTGLITTTSRKLDREQQAHEFLEVTVTDGGPSPKQSTIWVVVQVLDENDNKPQFPEKVYQ
LEX  KTGLITTTSRKLDREQQAHEFLEVTVTDGGPSPKQSTIWVVVQVLDENDNKPQFPEKVYQ
          1200      1210      1220      1230      1240      1250

          1270      1280      1290      1300      1310      1320
LEX  IKLPERDRKKRGEPIYRAFAFDRDEGPNAEISYSIVDGNDDGKFFIDPKTGMVSSRKQFT
LEX  IKLPERDRKKRGEPIYRAFAFDRDEGPNAEISYSIVDGNDDGKFFIDPKTGMVSSRKQFT
          1260      1270      1280      1290      1300      1310

          1330      1340      1350      1360      1370      1380
LEX  AGSYDILTIKAVDNGRPQKSSTARLHIEWIKKPPPSPIPLTFDEPFYNFTVMESDRVTEI
LEX  AGSYDILTIKAVDNGRPQKSSTARLHIEWIKKPPPSPIPLTFDEPFYNFTVMESDRVTEI
          1320      1330      1340      1350      1360      1370

          1390      1400      1410      1420      1430      1440
LEX  VGVVSVQPANTPLWFDIVGGNFDSAFDAEKGVTIVIAKPLDAEQRSIYNMSVEVTDGTN
LEX  VGVVSVQPANTPLWFDIVGGNFDSAFDAEKGVTIVIAKPLDAEQRSIYNMSVEVTDGTN
          1380      1390      1400      1410      1420      1430

          1450      1460      1470      1480      1490      1500
LEX  VAVTQVFIKVLNNDNGPEFSQPNYDVTISEDVLPDTEILQIEATDRDEKHKLSYTVHSS
LEX  VAVTQVFIKVLNNDNGPEFSQPNYDVTISEDVLPDTEILQIEATDRDEKHKLSYTVHSS
          1440      1450      1460      1470      1480      1490

          1510      1520      1530      1540      1550      1560
LEX  IDSISMRKFRIDPSTGVLTYAERLDHEAQDKHILNIMVRDQEFPPYRRNLARVIVNVEDAN
LEX  IDSISMRKFRIDPSTGVLTYAERLDHEAQDKHILNIMVRDQEFPPYRRNLARVIVNVEDAN
          1500      1510      1520      1530      1540      1550
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      1570      1580      1590      1600      1610      1620
LEX   DHSPYFTNPLYEASVFESAALGSAVLQVTALDKDKGENAELIYTIEAGNTGNMFKIEPVL
      .....
LEX   DHSPYFTNPLYEASVFESAALGSAVLQVTALDKDKGENAELIYTIEAGNTGNMFKIEPVL
      1560      1570      1580      1590      1600      1610

      1630      1640      1650      1660      1670      1680
LEX   GIITICKEPDMTTMGQFVLSIKVTDQGSPPMSATAIVRISVTMSDN SHPKFIHKDYQAEV
      .....
LEX   GIITICKEPDMTTMGQFVLSIKVTDQGSPPMSATAIVRISVTMSDN SHPKFIHKDYQAEV
      1620      1630      1640      1650      1660      1670

      1690      1700      1710      1720      1730      1740
LEX   NENVDIGTSVILISAIQSSTLIYEVKDG DINGIFTINPYSGVITTQKALDYERTSSYQLI
      .....
LEX   NENVDIGTSVILISAIQSSTLIYEVKDG DINGIFTINPYSGVITTQKALDYERTSSYQLI
      1680      1690      1700      1710      1720      1730

      1750      1760      1770      1780      1790      1800
LEX   IQATNMAGMASNATVNIQIVDENDNAPVFLFSQYSGSLSEAAPINSIVRSLDNSPLVIRA
      .....
LEX   IQATNMAGMASNATVNIQIVDENDNAPVFLFSQYSGSLSEAAPINSIVRSLDNSPLVIRA
      1740      1750      1760      1770      1780      1790

      1810      1820      1830      1840      1850      1860
LEX   TDADSNRNALLVYQIVESTAKKFFTVD SSTGAIRTIANLDHETIAHFHFHVHVRDSGSPQ
      .....
LEX   TDADSNRNALLVYQIVESTAKKFFTVD SSTGAIRTIANLDHETIAHFHFHVHVRDSGSPQ
      1800      1810      1820      1830      1840      1850

      1870      1880      1890      1900      1910      1920
LEX   LTAESPVEVNIEVTDVNDNPPVFTQAVFETILL LPTYVGVEVLKVSATDPDSEVPPELTY
      .....
LEX   LTAESPVEVNIEVTDVNDNPPVFTQAVFETILL LPTYVGVEVLKVSATDPDSEVPPELTY
      1860      1870      1880      1890      1900      1910

      1930      1940      1950      1960      1970      1980
LEX   SLMEGSLDHFLIDSNSGVLTIKNNNLSKDH YMLIVKVSDGKFYSTSMVTIMVKEAMDSGL
      .....
LEX   SLMEGSLDHFLIDSNSGVLTIKNNNLSKDH YMLIVKVSDGKFYSTSMVTIMVKEAMDSGL
      1920      1930      1940      1950      1960      1970

      1990      2000      2010      2020      2030      2040
LEX   HFTQSFYSTSISENNTNITKVAIVNAVGNRL NEPLKYSILNPGNKFKIKSTSGVIQTTGV
      .....
LEX   HFTQSFYSTSISENNTNITKVAIVNAVGNRL NEPLKYSILNPGNKFKIKSTSGVIQTTGV
      1980      1990      2000      2010      2020      2030

      2050      2060      2070      2080      2090      2100
LEX   PFDREEQELYELVVEASRELDHLRVARVVVRV NIEDINDNSPVFVGLPYAAVQVDAEPG
      .....
LEX   PFDREEQELYELVVEASRELDHLRVARVVVRV NIEDINDNSPVFVGLPYAAVQVDAEPG
      2040      2050      2060      2070      2080      2090

      2110      2120      2130      2140      2150      2160
LEX   TLIYQVTAIDKDKGPNGEVTYVLQDDYGHFEI NPNSGNVILKEAFNSDLSNIEYGVVILA
      .....
LEX   TLIYQVTAIDKDKGPNGEVTYVLQDDYGHFEI NPNSGNVILKEAFNSDLSNIEYGVVILA
      2100      2110      2120      2130      2140      2150
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      2170      2180      2190      2200      2210      2220
LEX  KDGGKPSLSTSVELPITIVNKAMPVFDKPFYTASVNEDIRMNTPILSINATSPEGQGIY
      .....
LEX  KDGGKPSLSTSVELPITIVNKAMPVFDKPFYTASVNEDIRMNTPILSINATSPEGQGIY
      2160      2170      2180      2190      2200      2210

      2230      2240      2250      2260      2270      2280
LEX  IIIDGDPFKQFNIDFDTGVLKVVSPLDYEVTSAAYKLTIASDALTGARA EVTVDLLVNDV
      .....
LEX  IIIDGDPFKQFNIDFDTGVLKVVSPLDYEVTSAAYKLTIASDALTGARA EVTVDLLVNDV
      2220      2230      2240      2250      2260      2270

      2290      2300      2310      2320      2330      2340
LEX  NDNPPIFDQPTYNTTLSEASLIGTPVLQVVSIDADSENNKMHYQIVQDTYNSTDYFHID
      .....
LEX  NDNPPIFDQPTYNTTLSEASLIGTPVLQVVSIDADSENNKMHYQIVQDTYNSTDYFHID
      2280      2290      2300      2310      2320      2330

      2350      2360      2370      2380      2390      2400
LEX  SSSGLILTARMLDHELVQHCTLKVRSIDSGFSPSLSEVLVHIYISDVNDNPPVFNQLIYE
      .....
LEX  SSSGLILTARMLDHELVQHCTLKVRSIDSGFSPSLSEVLVHIYISDVNDNPPVFNQLIYE
      2340      2350      2360      2370      2380      2390

      2410      2420      2430      2440      2450      2460
LEX  SYVSELAPRGHFVTCVQASDADSSDFDRLEYSILSGNDRTSFLMDSKSGVITLSNHRKQR
      .....
LEX  SYVSELAPRGHFVTCVQASDADSSDFDRLEYSILSGNDRTSFLMDSKSGVITLSNHRKQR
      2400      2410      2420      2430      2440      2450

      2470      2480      2490      2500      2510      2520
LEX  MEPLYSNLVSVSDGLFTSTAQVHIRVLGANLYSPAFSQSTYVAEVRENVAAGTKVIHVRA
      .....
LEX  MEPLYSNLVSVSDGLFTSTAQVHIRVLGANLYSPAFSQSTYVAEVRENVAAGTKVIHVRA
      2460      2470      2480      2490      2500      2510

      2530      2540      2550      2560      2570      2580
LEX  TDGDPGTGQISYAIINDFAKDRFLIDSNQVITTELDRENPLEGDVSIFVRALDGGGR
      .....
LEX  TDGDPGTGQISYAIINDFAKDRFLIDSNQVITTELDRENPLEGDVSIFVRALDGGGR
      2520      2530      2540      2550      2560      2570

      2590      2600      2610      2620      2630      2640
LEX  TTFCTVRVIVVDENDNAPQFMTEYRASVRADVGRGHLVTQVQAIDPDDGANSRITYSLY
      .....
LEX  TTFCTVRVIVVDENDNAPQFMTEYRASVRADVGRGHLVTQVQAIDPDDGANSRITYSLY
      2580      2590      2600      2610      2620      2630

      2650      2660      2670      2680      2690      2700
LEX  SEASVSVADLLEIDPDNGWMVTKGNFNQLKNTVLSFFVKAVDGGIPVKHSLIPVYIHVLP
      .....
LEX  SEASVSVADLLEIDPDNGWMVTKGNFNQLKNTVLSFFVKAVDGGIPVKHSLIPVYIHVLP
      2640      2650      2660      2670      2680      2690

      2710      2720      2730      2740      2750      2760
LEX  PETFLPSFTQSQYSFTIAEDTAIGSTVDTLRILPSQNVWFSTVNGERPENNKGGVFVIEQ
      .....
LEX  PETFLPSFTQSQYSFTIAEDTAIGSTVDTLRILPSQNVWFSTVNGERPENNKGGVFVIEQ
      2700      2710      2720      2730      2740      2750
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      2770      2780      2790      2800      2810      2820
LEX  ETGTIKLDKRLDRETSPAFHFKVAATIPLDKVDIVFTVDVDIKVLDLNDNKPVFETSSYD
      .....
LEX  ETGTIKLDKRLDRETSPAFHFKVAATIPLDKVDIVFTVDVDIKVLDLNDNKPVFETSSYD
2760      2770      2780      2790      2800      2810

      2830      2840      2850      2860      2870      2880
LEX  TIIMEGMPVGTCLTQVRAIDMDWGANGQVTYSLHSDSQPEKVMFAFNIDSNTGWISTLKD
      .....
LEX  TIIMEGMPVGTCLTQVRAIDMDWGANGQVTYSLHSDSQPEKVMFAFNIDSNTGWISTLKD
2820      2830      2840      2850      2860      2870

      2890      2900      2910      2920      2930      2940
LEX  LDHETDPTFTFSVVASDLGEAFSLSSSTALVSVRVTDINDNAPVFAQEVYRGNVKESDPPG
      .....
LEX  LDHETDPTFTFSVVASDLGEAFSLSSSTALVSVRVTDINDNAPVFAQEVYRGNVKESDPPG
2880      2890      2900      2910      2920      2930

      2950      2960      2970      2980      2990      3000
LEX  EVVAVLSTWDRDTSVDNRQVSYHITGGNPRGRFALGLVQSEWKVYVKRPLDREEQDIYFL
      .....
LEX  EVVAVLSTWDRDTSVDNRQVSYHITGGNPRGRFALGLVQSEWKVYVKRPLDREEQDIYFL
2940      2950      2960      2970      2980      2990

      3010      3020      3030      3040      3050      3060
LEX  NITATDGLFVTQAMVEVSVDVNDNSPVCQVAYTALLPEDIPSNKIILKVSADKADIGS
      .....
LEX  NITATDGLFVTQAMVEVSVDVNDNSPVCQVAYTALLPEDIPSNKIILKVSADKADIGS
3000      3010      3020      3030      3040      3050

      3070      3080      3090      3100      3110      3120
LEX  NGYIRYSLYSGNSEFFLDPESELKTLALLDRERIPVYSLMAKATDGGGRFCQSNHILI
      .....
LEX  NGYIRYSLYSGNSEFFLDPESELKTLALLDRERIPVYSLMAKATDGGGRFCQSNHILI
3060      3070      3080      3090      3100      3110

      3130      3140      3150      3160      3170      3180
LEX  LEDVNDNPPVFSSDHYNTCVYENTATKALLTRVQAVDPDIGINRKVVYSLADSAGGVFSI
      .....
LEX  LEDVNDNPPVFSSDHYNTCVYENTATKALLTRVQAVDPDIGINRKVVYSLADSAGGVFSI
3120      3130      3140      3150      3160      3170

      3190      3200      3210      3220      3230      3240
LEX  DSSSGIILEQPLDREQQSSYNISVRATDQSPGQSLSSLTTVTITVLDINDNPPVFERRD
      .....
LEX  DSSSGIILEQPLDREQQSSYNISVRATDQSPGQSLSSLTTVTITVLDINDNPPVFERRD
3180      3190      3200      3210      3220      3230

      3250      3260      3270      3280      3290      3300
LEX  YLVTVPEDTSPGTQVLAVFATSKDIGTNAEITYLIRSGNEQGKFKINPKTGGISVSEVLD
      .....
LEX  YLVTVPEDTSPGTQVLAVFATSKDIGTNAEITYLIRSGNEQGKFKINPKTGGISVSEVLD
3240      3250      3260      3270      3280      3290

      3310      3320      3330      3340      3350      3360
LEX  YELCKRFYLVVEAKDGGTPALSAVATVNINLTDVNDNPPKFSQDVYSAVISEDALVGDSV
      .....
LEX  YELCKRFYLVVEAKDGGTPALSAVATVNINLTDVNDNPPKFSQDVYSAVISEDALVGDSV
3300      3310      3320      3330      3340      3350
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      3370      3380      3390      3400      3410      3420
LEX  ILLIAEDVDSQPNGQIHFSIVNGDRDNEFTVDPVLGLVKVKKKLDREVRSGYSLLVQAVD
      .....
LEX  ILLIAEDVDSQPNGQIHFSIVNGDRDNEFTVDPVLGLVKVKKKLDREVRSGYSLLVQAVD
      3360      3370      3380      3390      3400      3410

      3430      3440      3450      3460      3470      3480
LEX  SGIPAMSSTATVNIDISDVNDNSPVFTFANYTAVIQENKPVGTSILQLVVTDRDSFHNGP
      .....
LEX  SGIPAMSSTATVNIDISDVNDNSPVFTFANYTAVIQENKPVGTSILQLVVTDRDSFHNGP
      3420      3430      3440      3450      3460      3470

      3490      3500      3510      3520      3530      3540
LEX  PFSFSILSGNEEEFVLDPHGILRSVAVVFQHTESLEYVLCVQAKDSGKPPQVSHTYIRVR
      .....
LEX  PFSFSILSGNEEEFVLDPHGILRSVAVVFQHTESLEYVLCVQAKDSGKPPQVSHTYIRVR
      3480      3490      3500      3510      3520      3530

      3550      3560      3570      3580      3590      3600
LEX  VIEESTHKPTAIPLEIFIVTMEDDFPGGVIGKIHATDQDMYDVLTFALKSEQKSLFKVNS
      .....
LEX  VIEESTHKPTAIPLEIFIVTMEDDFPGGVIGKIHATDQDMYDVLTFALKSEQKSLFKVNS
      3540      3550      3560      3570      3580      3590

      3610      3620      3630      3640      3650      3660
LEX  HDGKIIALGGLDSGKYVLNVSVSDGRFQVPIDVVHVEQLVHEMLQNTVTIRFENVSPED
      .....
LEX  HDGKIIALGGLDSGKYVLNVSVSDGRFQVPIDVVHVEQLVHEMLQNTVTIRFENVSPED
      3600      3610      3620      3630      3640      3650

      3670      3680      3690      3700      3710      3720
LEX  FVGLHMHGFRRTLRLNAVLTQKQDSLRIISIQPVAGTNQLDMLFAVEMHSSEFYKPAYLIQ
      .....
LEX  FVGLHMHGFRRTLRLNAVLTQKQDSLRIISIQPVAGTNQLDMLFAVEMHSSEFYKPAYLIQ
      3660      3670      3680      3690      3700      3710

      3730      3740      3750      3760      3770      3780
LEX  KLSNARRHLENIMRISAILEKNCSGLDCQEQHCEQGLSLDSHALMTYSTARISFVCPRFY
      .....
LEX  KLSNARRHLENIMRISAILEKNCSGLDCQEQHCEQGLSLDSHALMTYSTARISFVCPRFY
      3720      3730      3740      3750      3760      3770

      3790      3800      3810      3820      3830      3840
LEX  RNVRCCTCNGGLCPGSNDPCVEKPCPGDMQCVGYEASRRPFLCQCPPGKLGECSGHTSLSF
      .....
LEX  RNVRCCTCNGGLCPGSNDPCVEKPCPGDMQCVGYEASRRPFLCQCPPGKLGECSGHTSLSF
      3780      3790      3800      3810      3820      3830

      3850      3860      3870      3880      3890      3900
LEX  AGNSYIKYRLSENSKEEDFKLALRLRTLQSNGIIMYTRANPCIILKIVDGKLWFLDCGS
      .....
LEX  AGNSYIKYRLSENSKEEDFKLALRLRTLQSNGIIMYTRANPCIILKIVDGKLWFLDCGS
      3840      3850      3860      3870      3880      3890

      3910      3920      3930      3940      3950      3960
LEX  GPGILGISGRAVNDGWSVFLNLRNFTSLSLDDSYVERRRAPLYFQTLSTESSIYFGA
      .....
LEX  GPGILGISGRAVNDGWSVFLNLRNFTSLSLDDSYVERRRAPLYFQTLSTESSIYFGA
      3900      3910      3920      3930      3940      3950
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      3970      3980      3990      4000      4010      4020
LEX  LVQADNIRSLTDRVTQVLSGFQGC LDSVILNNNELPLQNKRSSFAEVVGLTELKLGCVL
      .....
LEX  LVQADNIRSLTDRVTQVLSGFQGC LDSVILNNNELPLQNKRSSFAEVVGLTELKLGCVL
3960      3970      3980      3990      4000      4010

      4030      4040      4050      4060      4070      4080
LEX  YPDACKRSPCQHGGSGCTGLPSGGYQCTCLSQFTGRNCESEITACFPNPCRNGGSCDPIGN
      .....
LEX  YPDACKRSPCQHGGSGCTGLPSGGYQCTCLSQFTGRNCESEITACFPNPCRNGGSCDPIGN
4020      4030      4040      4050      4060      4070

      4090      4100      4110      4120      4130      4140
LEX  TFICNCKAGLTGVTCEEDINECERECEENGSGCVNVFGSFLCNCTPGYVGQYCGLRPVVV
      .....
LEX  TFICNCKAGLTGVTCEEDINECERECEENGSGCVNVFGSFLCNCTPGYVGQYCGLRPVVV
4080      4090      4100      4110      4120      4130

      4150      4160      4170      4180      4190      4200
LEX  PNIQAGHSYVGKEELIGIAVVLVLFVIFILVVLVLFVFRKKVFRKNYSRNNITLVQDPATAAL
      .....
LEX  PNIQAGHSYVGKEELIGIAVVLVLFVIFILVVLVLFVFRKKVFRKNYSRNNITLVQDPATAAL
4140      4150      4160      4170      4180      4190

      4210      4220      4230      4240      4250      4260
LEX  LNKSNGIPFRNLRGSGDGRNVYQEVGPPQVPVRPMAYTPCFQSDSRSNLDKIVDGLGGEH
      .....
LEX  LNKSNGIPFRNLRGSGDGRNVYQEVGPPQVPVRPMAYTPCFQSDSRSNLDKIVDGLGGEH
4200      4210      4220      4230      4240      4250

      4270      4280      4290      4300      4310      4320
LEX  QEMTTFHPESPRIILTARRGVVVC SVAPNLPAVSPCRSDCDSIRKNGWDAGTENKGVDDPG
      .....
LEX  QEMTTFHPESPRIILTARRGVVVC SVAPNLPAVSPCRSDCDSIRKNGWDAGTENKGVDDPG
4260      4270      4280      4290      4300      4310

      4330      4340      4350      4360      4370      4380
LEX  EVTCFAGSNKGSNSEQSLSSFQSDSGDDNASIVTVIQLVNNVVDTIENEVSVMDDQGGQNY
      .....
LEX  EVTCFAGSNKGSNSEQSLSSFQSDSGDDNASIVTVIQLVNNVVDTIENEVSVMDDQGGQNY
4320      4330      4340      4350      4360      4370

      4390      4400      4410      4420      4430      4440
LEX  NRAYHWDTSDWMPGARLSDIEEVPNYENQDGGSAHQGSTRELESYYLGGYDIDSEYPPP
      .....
LEX  NRAYHWDTSDWMPGARLSDIEEVPNYENQDGGSAHQGSTRELESYYLGGYDIDSEYPPP
4380      4390      4400      4410      4420      4430

      4450      4460      4470      4480      4490      4500
LEX  HEEEFSLSQDQLPPPLPEDFPDQYEALPPSQPVSLASTLSPDCRRRPQFHPSQYLPHPHFP
      .....
LEX  HEEEFSLSQDQLPPPLPEDFPDQYEALPPSQPVSLASTLSPDCRRRPQFHPSQYLPHPHFP
4440      4450      4460      4470      4480      4490

      4510      4520      4530      4540      4550      4560
LEX  NETDLVGPPASCEFSTFAVSMNQTEPTGPADSVSLSLHNSRGTS SSSDVSANCGFDDSEV
      .....
LEX  NETDLVGPPASCEFSTFAVSMNQTEPTGPADSVSLSLHNSRGTS SSSDVSANCGFDDSEV
4500      4510      4520      4530      4540      4550
```

```
          4570      4580
LEX   AMSDYESVGELSLASLHIPFVETQHQTQV
      ::::::::::::::::::::::::::::
LEX   AMSDYESVGELSLASLHIPFVETQHQTQV
      4560      4570      4580
```

4589 residues in 1 query sequences

4585 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Tue Oct 21 17:25:39 2003 done: Tue Oct 21 17:25:58 2003

Scan time: 0.200 Display time: 30.350

Function used was FASTA

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAIfaG21: 4589 aa

>LEX 285 SEQ ID NO:2

vs /tmp/fastaDAAJfaG21 library

searching /tmp/fastaDAAJfaG21 library

3852 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2

join: 51, opt: 39, gap-pen: -12/ -2, width: 16

Scan time: 0.134

The best scores are:

opt

LEX 285 SEQ ID NO:4

(3852) 24961

>>LEX 285 SEQ ID NO:4

(3852 aa)

initn: 24961 initl: 24961 opt: 24961

Smith-Waterman score: 24961; 100.000% identity in 3852 aa overlap (1-3852:1-3852)

	10	20	30	40	50	60
LEX	MDIIMGHC	VGTRPPAC	LILLFLK	LLATVSQ	GLPGTG	PLGFHFTH
LEX	MDIIMGHC	VGTRPPAC	LILLFLK	LLATVSQ	GLPGTG	PLGFHFTH
	10	20	30	40	50	60
	70	80	90	100	110	120
LEX	YVNSQSR	MGITLID	LSWDIKY	RIVSGDE	EFGFKAE	EVIIADFC
LEX	YVNSQSR	MGITLID	LSWDIKY	RIVSGDE	EFGFKAE	EVIIADFC
	70	80	90	100	110	120
	130	140	150	160	170	180
LEX	IQDNYLL	LIVKGS	VRGEDLE	AWTKVNI	QVLDMND	LRPLFSPT
LEX	IQDNYLL	LIVKGS	VRGEDLE	AWTKVNI	QVLDMND	LRPLFSPT
	130	140	150	160	170	180
	190	200	210	220	230	240
LEX	TATDADIG	SNGEFY	YFKNKVD	LFSVHPT	SGVISLS	SGRLNYDE
LEX	TATDADIG	SNGEFY	YFKNKVD	LFSVHPT	SGVISLS	SGRLNYDE
	190	200	210	220	230	240
	250	260	270	280	290	300
LEX	YGNGVSS	TAKLYV	HIERINE	HAPTIVV	THVPFSL	EKEPTYAV
LEX	YGNGVSS	TAKLYV	HIERINE	HAPTIVV	THVPFSL	EKEPTYAV
	250	260	270	280	290	300
	310	320	330	340	350	360
LEX	VSIVAGD	PLDQFF	LAKEGK	WLNEYKI	KERKQID	WESFPYGY
LEX	VSIVAGD	PLDQFF	LAKEGK	WLNEYKI	KERKQID	WESFPYGY
	310	320	330	340	350	360

```

      370      380      390      400      410      420
LEX  AVYIGNPTRDTPVPIRFEKEVYDVSISEFSPPGVVVAIVKLSPEPIDVEYKLSPGEDAVYF
      .....
LEX  AVYIGNPTRDTPVPIRFEKEVYDVSISEFSPPGVVVAIVKLSPEPIDVEYKLSPGEDAVYF
      370      380      390      400      410      420

      430      440      450      460      470      480
LEX  KINPRSGLIVTARPLNTVKKEVYKLEVTNKEGDLKAQVTISIEDANDHTPEFQQPLYDAY
      .....
LEX  KINPRSGLIVTARPLNTVKKEVYKLEVTNKEGDLKAQVTISIEDANDHTPEFQQPLYDAY
      430      440      450      460      470      480

      490      500      510      520      530      540
LEX  VNESVPVGTSVLTVSASDKDKGENGYITYSIALNLLPFVINQFTGVISTTEELDFESSP
      .....
LEX  VNESVPVGTSVLTVSASDKDKGENGYITYSIALNLLPFVINQFTGVISTTEELDFESSP
      490      500      510      520      530      540

      550      560      570      580      590      600
LEX  EIYRFIVRASDWGSPYRHESEVNVITIRIGNVNDNSPLFEKVACQGVISYDFPVGGHITAV
      .....
LEX  EIYRFIVRASDWGSPYRHESEVNVITIRIGNVNDNSPLFEKVACQGVISYDFPVGGHITAV
      550      560      570      580      590      600

      610      620      630      640      650      660
LEX  SAIDIDELELVKYKIIISGNELGFFYLNPDSGVLQLKKSLTNSGIKNGNFALRITATDGEN
      .....
LEX  SAIDIDELELVKYKIIISGNELGFFYLNPDSGVLQLKKSLTNSGIKNGNFALRITATDGEN
      610      620      630      640      650      660

      670      680      690      700      710      720
LEX  LADPMSINISVLHGKVSSKSFSCRETRVAQKLAEKLLIKAKANGKLNLEDGFLDFYSINR
      .....
LEX  LADPMSINISVLHGKVSSKSFSCRETRVAQKLAEKLLIKAKANGKLNLEDGFLDFYSINR
      670      680      690      700      710      720

      730      740      750      760      770      780
LEX  QGPYFDKSFPSDVAVKEDLPVGANILKIKAYDADSGFNGKVLFTISDGNTDSCFNIDMET
      .....
LEX  QGPYFDKSFPSDVAVKEDLPVGANILKIKAYDADSGFNGKVLFTISDGNTDSCFNIDMET
      730      740      750      760      770      780

      790      800      810      820      830      840
LEX  GQLKVLMPMDREHTDLYLLNITIYDLGNPQKSSWRLLTINVEDANDNSPVFIQDSYSVNI
      .....
LEX  GQLKVLMPMDREHTDLYLLNITIYDLGNPQKSSWRLLTINVEDANDNSPVFIQDSYSVNI
      790      800      810      820      830      840

      850      860      870      880      890      900
LEX  LESSGIGTEIIQVEARDKDLGSNGEVTYSVLTDTQQFAINSSTGIVYVADQLDRESKANY
      .....
LEX  LESSGIGTEIIQVEARDKDLGSNGEVTYSVLTDTQQFAINSSTGIVYVADQLDRESKANY
      850      860      870      880      890      900

      910      920      930      940      950      960
LEX  SLKIEARDKAESGQQLFSVVTCLKVFLDDVND CSPAFIPSSYSVKVLEDLPVGTVIAWLET
      .....
LEX  SLKIEARDKAESGQQLFSVVTCLKVFLDDVND CSPAFIPSSYSVKVLEDLPVGTVIAWLET
      910      920      930      940      950      960
```

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      970      980      990      1000      1010      1020
LEX  HDPDLGLGGQVRYSLVNDYNGRFEIDKASGAIRLSKELDYEQQFYNLTVRAKDKGRPV
LEX  HDPDLGLGGQVRYSLVNDYNGRFEIDKASGAIRLSKELDYEQQFYNLTVRAKDKGRPV
      970      980      990      1000      1010      1020

      1030      1040      1050      1060      1070      1080
LEX  LSSVSFVEVEVVDVNNENLHTPYFPDFAVVGSVKENSRIGHTSVLQVTARDEDSGRDGEIQY
LEX  LSSVSFVEVEVVDVNNENLHTPYFPDFAVVGSVKENSRIGHTSVLQVTARDEDSGRDGEIQY
      1030      1040      1050      1060      1070      1080

      1090      1100      1110      1120      1130      1140
LEX  SIRDGSGLGGRFSIDDESGVITAADILDRETMGSYWLTVYATDRGVVPLYSTIEVYIEVED
LEX  SIRDGSGLGGRFSIDDESGVITAADILDRETMGSYWLTVYATDRGVVPLYSTIEVYIEVED
      1090      1100      1110      1120      1130      1140

      1150      1160      1170      1180      1190      1200
LEX  VNDNAPLTSEPIIYPVVMENSPKDVSVIQUIAEDPDSSSNEKLTYRITSGNPQNFFAINI
LEX  VNDNAPLTSEPIIYPVVMENSPKDVSVIQUIAEDPDSSSNEKLTYRITSGNPQNFFAINI
      1150      1160      1170      1180      1190      1200

      1210      1220      1230      1240      1250      1260
LEX  KTGLITTTSRKLDREQQAEHFLEVTVDGGSPKQSTIWVVVQVLDENDNKPQFPEKVYQ
LEX  KTGLITTTSRKLDREQQAEHFLEVTVDGGSPKQSTIWVVVQVLDENDNKPQFPEKVYQ
      1210      1220      1230      1240      1250      1260

      1270      1280      1290      1300      1310      1320
LEX  IKLPERDRKKRGEPIYRAFAFDRDEGPNAEISYSIVDGNDDGKFFIDPKTGMVSSRKQFT
LEX  IKLPERDRKKRGEPIYRAFAFDRDEGPNAEISYSIVDGNDDGKFFIDPKTGMVSSRKQFT
      1270      1280      1290      1300      1310      1320

      1330      1340      1350      1360      1370      1380
LEX  AGSYDILTIKAVDNGRPQKSSTARLHIEWIKKPPPSPIPLTFDEPFYNFTVMESDRVTEI
LEX  AGSYDILTIKAVDNGRPQKSSTARLHIEWIKKPPPSPIPLTFDEPFYNFTVMESDRVTEI
      1330      1340      1350      1360      1370      1380

      1390      1400      1410      1420      1430      1440
LEX  VGVVSVQPANTPLWFDIVGGNFDSAFDAEKGVTIVIAKPLDAEQRSIYNMSVEVTDGTN
LEX  VGVVSVQPANTPLWFDIVGGNFDSAFDAEKGVTIVIAKPLDAEQRSIYNMSVEVTDGTN
      1390      1400      1410      1420      1430      1440

      1450      1460      1470      1480      1490      1500
LEX  VAVTQVFIKVLNNDNGPEFSQPNYDVTISEDVLPDTEILQIEATDRDEKHKLSYTVHSS
LEX  VAVTQVFIKVLNNDNGPEFSQPNYDVTISEDVLPDTEILQIEATDRDEKHKLSYTVHSS
      1450      1460      1470      1480      1490      1500

      1510      1520      1530      1540      1550      1560
LEX  IDSISMRKFRIDPSTGVLYTAERLDHEAQDKHILNIMVRDQEFPYRRNLARVIVNVEDAN
LEX  IDSISMRKFRIDPSTGVLYTAERLDHEAQDKHILNIMVRDQEFPYRRNLARVIVNVEDAN
      1510      1520      1530      1540      1550      1560
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1570      1580      1590      1600      1610      1620
LEX DHSPYFTNPLYEASVFESAALGSAVLQVTALDKDKGENAELIYTIEAGNTGNMFKIEPVL
LEX DHSPYFTNPLYEASVFESAALGSAVLQVTALDKDKGENAELIYTIEAGNTGNMFKIEPVL
1570      1580      1590      1600      1610      1620

1630      1640      1650      1660      1670      1680
LEX GIITICKEPDMTTMGQFVLSIKVTDQGSPMSATAIVRISVTMSDN SHPKFIHKDYQAEV
LEX GIITICKEPDMTTMGQFVLSIKVTDQGSPMSATAIVRISVTMSDN SHPKFIHKDYQAEV
1630      1640      1650      1660      1670      1680

1690      1700      1710      1720      1730      1740
LEX NENVDIGTSVILISAI SQSTLIYE VKDGDINGIFTINPYSGVITTQKALDYERTSSYQLI
LEX NENVDIGTSVILISAI SQSTLIYE VKDGDINGIFTINPYSGVITTQKALDYERTSSYQLI
1690      1700      1710      1720      1730      1740

1750      1760      1770      1780      1790      1800
LEX IQATNMAGMASNATVNIQIVDENDNAPVFLFSQYSGSLSEAAPINSIVRSLDNSPLVIRA
LEX IQATNMAGMASNATVNIQIVDENDNAPVFLFSQYSGSLSEAAPINSIVRSLDNSPLVIRA
1750      1760      1770      1780      1790      1800

1810      1820      1830      1840      1850      1860
LEX TDADSNRNALLVYQIVESTAKKFFTVD SSTGAIRTIANLDHETIAHFHFHVHVRDSGSPQ
LEX TDADSNRNALLVYQIVESTAKKFFTVD SSTGAIRTIANLDHETIAHFHFHVHVRDSGSPQ
1810      1820      1830      1840      1850      1860

1870      1880      1890      1900      1910      1920
LEX LTAESPVEVNIEVTDVNDNPPVFTQAVFETILLPT YVGVEVLKVSATDPDSEVPPELTY
LEX LTAESPVEVNIEVTDVNDNPPVFTQAVFETILLPT YVGVEVLKVSATDPDSEVPPELTY
1870      1880      1890      1900      1910      1920

1930      1940      1950      1960      1970      1980
LEX SLMEGSLDHFLIDSNSGVLTIKNNNLSKDHYMLIVKVSDGKFYSTSMVTIMVKEAMDSGL
LEX SLMEGSLDHFLIDSNSGVLTIKNNNLSKDHYMLIVKVSDGKFYSTSMVTIMVKEAMDSGL
1930      1940      1950      1960      1970      1980

1990      2000      2010      2020      2030      2040
LEX HFTQSFYSTSISENNITKVAIVNAVGNRLNEPLKYSILNPGNKFKIKSTSGVIQTTGV
LEX HFTQSFYSTSISENNITKVAIVNAVGNRLNEPLKYSILNPGNKFKIKSTSGVIQTTGV
1990      2000      2010      2020      2030      2040

2050      2060      2070      2080      2090      2100
LEX PFDREEQELYELVVEASRELDHLRVARVVVRVNIEDINDNSPVFVGLPYAAVQVDAEPG
LEX PFDREEQELYELVVEASRELDHLRVARVVVRVNIEDINDNSPVFVGLPYAAVQVDAEPG
2050      2060      2070      2080      2090      2100

2110      2120      2130      2140      2150      2160
LEX TLIYQVTAIDKDKGPNGEVTYVLQDDYGHFEINPNSGNVILKEAFNSDLSNIEYGV TILA
LEX TLIYQVTAIDKDKGPNGEVTYVLQDDYGHFEINPNSGNVILKEAFNSDLSNIEYGV TILA
2110      2120      2130      2140      2150      2160
```

	2170	2180	2190	2200	2210	2220
LEX	KDGGKPSLSTSVELPITIVNKAMPVFDKPFYTASVNEDIRMNTPILSINATSPEGQGIY					
	2170	2180	2190	2200	2210	2220
LEX	KDGGKPSLSTSVELPITIVNKAMPVFDKPFYTASVNEDIRMNTPILSINATSPEGQGIY					
	2230	2240	2250	2260	2270	2280
LEX	IIIDGDPFKQFNIDFDTGVLKVVSPLDYEVTSAYKLTIRASDALTGARAEVTVDLLVNDV					
	2230	2240	2250	2260	2270	2280
LEX	IIIDGDPFKQFNIDFDTGVLKVVSPLDYEVTSAYKLTIRASDALTGARAEVTVDLLVNDV					
	2290	2300	2310	2320	2330	2340
LEX	NDNPPIFDQPTYNTTLSEASLIGTPVLQVVSIDADSENNKMVHYQIVQDTYNSTDYFHID					
	2290	2300	2310	2320	2330	2340
LEX	NDNPPIFDQPTYNTTLSEASLIGTPVLQVVSIDADSENNKMVHYQIVQDTYNSTDYFHID					
	2350	2360	2370	2380	2390	2400
LEX	SSSGLILTARMLDHELVQHCTLKVRSIDSGFPSLSSEVLVHIYISDVNDNPPVFNQLIYE					
	2350	2360	2370	2380	2390	2400
LEX	SSSGLILTARMLDHELVQHCTLKVRSIDSGFPSLSSEVLVHIYISDVNDNPPVFNQLIYE					
	2410	2420	2430	2440	2450	2460
LEX	SYVSELAPRGHFVTCVQASDADSSDFDRLEYSILSGNDRTSFLMDSKSGVITLSNHRKQR					
	2410	2420	2430	2440	2450	2460
LEX	SYVSELAPRGHFVTCVQASDADSSDFDRLEYSILSGNDRTSFLMDSKSGVITLSNHRKQR					
	2470	2480	2490	2500	2510	2520
LEX	MEPLYSLNVSVDGLFTSTAQVHIRVLGANLYSPAFSQSTYVAEVRENVAAGTKVIHVRA					
	2470	2480	2490	2500	2510	2520
LEX	MEPLYSLNVSVDGLFTSTAQVHIRVLGANLYSPAFSQSTYVAEVRENVAAGTKVIHVRA					
	2530	2540	2550	2560	2570	2580
LEX	TDGDPGTYGQISYAIINDFAKDRFLIDSNGQVITTERLDRENPLEGDVSIFVRALDGGGR					
	2530	2540	2550	2560	2570	2580
LEX	TDGDPGTYGQISYAIINDFAKDRFLIDSNGQVITTERLDRENPLEGDVSIFVRALDGGGR					
	2590	2600	2610	2620	2630	2640
LEX	TTFCTVRVIVVDENDNAPQFMTVEYRASVRADVGRGHLVTQVQAIDPDDGANSRITYSLY					
	2590	2600	2610	2620	2630	2640
LEX	TTFCTVRVIVVDENDNAPQFMTVEYRASVRADVGRGHLVTQVQAIDPDDGANSRITYSLY					
	2650	2660	2670	2680	2690	2700
LEX	SEASVSVADLLEIDPDNGWMVTKGNFNQLKNTVLSFFVKAVDGGIPVKHSLIPVYIHVLP					
	2650	2660	2670	2680	2690	2700
LEX	SEASVSVADLLEIDPDNGWMVTKGNFNQLKNTVLSFFVKAVDGGIPVKHSLIPVYIHVLP					
	2710	2720	2730	2740	2750	2760
LEX	PETFLPSFTQSQYSFTIAEDTAIGSTVDTLRILPSQNVWFSTVNGERPENNKGGVFVIEQ					
	2710	2720	2730	2740	2750	2760
LEX	PETFLPSFTQSQYSFTIAEDTAIGSTVDTLRILPSQNVWFSTVNGERPENNKGGVFVIEQ					

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      2770      2780      2790      2800      2810      2820
LEX   ETGTIKLDKRLDRETSPAFHFKVAATIPLDKVDIVFTVDVDIKVLDLNDNKPVFETSSYD
      .....
LEX   ETGTIKLDKRLDRETSPAFHFKVAATIPLDKVDIVFTVDVDIKVLDLNDNKPVFETSSYD
      2770      2780      2790      2800      2810      2820

      2830      2840      2850      2860      2870      2880
LEX   TIIMEGMPVGTKLTQVRAIDMDWGANGQVTYSLHSDSQPEKVMEAFNIDSNTGWISTLKD
      .....
LEX   TIIMEGMPVGTKLTQVRAIDMDWGANGQVTYSLHSDSQPEKVMEAFNIDSNTGWISTLKD
      2830      2840      2850      2860      2870      2880

      2890      2900      2910      2920      2930      2940
LEX   LDHETDPTFTFSVVASDLGEAFSLSSSTALVSVRVTDINDNAPVFAQEVYRGNVKESDPPG
      .....
LEX   LDHETDPTFTFSVVASDLGEAFSLSSSTALVSVRVTDINDNAPVFAQEVYRGNVKESDPPG
      2890      2900      2910      2920      2930      2940

      2950      2960      2970      2980      2990      3000
LEX   EVVAVLSTWDRDTSVDNRQVSYHITGGNPRGRFALGLVQSEWKVYVKRPLDREEQDIYFL
      .....
LEX   EVVAVLSTWDRDTSVDNRQVSYHITGGNPRGRFALGLVQSEWKVYVKRPLDREEQDIYFL
      2950      2960      2970      2980      2990      3000

      3010      3020      3030      3040      3050      3060
LEX   NITATDGLFVTQAMVEVSVSDVNDNSPVCQVAYTALLPEDIPSNKIILKVSADKADIGS
      .....
LEX   NITATDGLFVTQAMVEVSVSDVNDNSPVCQVAYTALLPEDIPSNKIILKVSADKADIGS
      3010      3020      3030      3040      3050      3060

      3070      3080      3090      3100      3110      3120
LEX   NGYIRYSLYGSGNSEFFLDPESELKTLALLDRERIPVYSLMAKATDGGGRFCQSNHILI
      .....
LEX   NGYIRYSLYGSGNSEFFLDPESELKTLALLDRERIPVYSLMAKATDGGGRFCQSNHILI
      3070      3080      3090      3100      3110      3120

      3130      3140      3150      3160      3170      3180
LEX   LEDVNDNPPVFSSDHYNTCVYENTATKALLTRVQAVDPDIGINRKVVYSLADSAGGVFSI
      .....
LEX   LEDVNDNPPVFSSDHYNTCVYENTATKALLTRVQAVDPDIGINRKVVYSLADSAGGVFSI
      3130      3140      3150      3160      3170      3180

      3190      3200      3210      3220      3230      3240
LEX   DSSSGIIILEQPLDREQQSSYNISVRATDQSPGQSLSSLTTVTITVLDINDNPPVFERRD
      .....
LEX   DSSSGIIILEQPLDREQQSSYNISVRATDQSPGQSLSSLTTVTITVLDINDNPPVFERRD
      3190      3200      3210      3220      3230      3240

      3250      3260      3270      3280      3290      3300
LEX   YLVTVPEDTSPGTQVLAVFATSKDIGTNAEITYLIRSGNEQGKFKINPKTGGISVSEVLD
      .....
LEX   YLVTVPEDTSPGTQVLAVFATSKDIGTNAEITYLIRSGNEQGKFKINPKTGGISVSEVLD
      3250      3260      3270      3280      3290      3300

      3310      3320      3330      3340      3350      3360
LEX   YELCKRFYLVVEAKDGGTPALSAVATVNINLTDVNDNPPKFSQDVYSAVISEDALVGDSV
      .....
LEX   YELCKRFYLVVEAKDGGTPALSAVATVNINLTDVNDNPPKFSQDVYSAVISEDALVGDSV
      3310      3320      3330      3340      3350      3360
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      3370      3380      3390      3400      3410      3420
LEX  ILLIAEDVDSQPNGQIHFSIVNGDRDNEFTVDPVLGLVKVKKKLDREVRVSGYSLLVQAVD
      .....
LEX  ILLIAEDVDSQPNGQIHFSIVNGDRDNEFTVDPVLGLVKVKKKLDREVRVSGYSLLVQAVD
      3370      3380      3390      3400      3410      3420

      3430      3440      3450      3460      3470      3480
LEX  SGIPAMSSTATVNIDISDVNDNSPVFTPANYTAVIQENKPVGTSILQLVVTDRDSFHNGP
      .....
LEX  SGIPAMSSTATVNIDISDVNDNSPVFTPANYTAVIQENKPVGTSILQLVVTDRDSFHNGP
      3430      3440      3450      3460      3470      3480

      3490      3500      3510      3520      3530      3540
LEX  PFSFSILSGNEEEFVLDPHGILRSVVFQHTESLEYVLCVQAKDSGKPPQVSHTYIRVR
      .....
LEX  PFSFSILSGNEEEFVLDPHGILRSVVFQHTESLEYVLCVQAKDSGKPPQVSHTYIRVR
      3490      3500      3510      3520      3530      3540

      3550      3560      3570      3580      3590      3600
LEX  VIEESTHKPTAIPLEIFIVTMEDDFPGGVIGKIHATDQDMYDVLTFALKSEQKSLFKVNS
      .....
LEX  VIEESTHKPTAIPLEIFIVTMEDDFPGGVIGKIHATDQDMYDVLTFALKSEQKSLFKVNS
      3550      3560      3570      3580      3590      3600

      3610      3620      3630      3640      3650      3660
LEX  HDGKIIALGGLDSGKYVLNVSVSDGRFQVPIDVVVHVEQLVHEMLQNTVTIRFENVSPED
      .....
LEX  HDGKIIALGGLDSGKYVLNVSVSDGRFQVPIDVVVHVEQLVHEMLQNTVTIRFENVSPED
      3610      3620      3630      3640      3650      3660

      3670      3680      3690      3700      3710      3720
LEX  FVGLHMHGFRRTLRLNAVLTKQKQDSLRIISIQPVAGTNQLDMLFAVEMHSSEFYKPAYLIQ
      .....
LEX  FVGLHMHGFRRTLRLNAVLTKQKQDSLRIISIQPVAGTNQLDMLFAVEMHSSEFYKPAYLIQ
      3670      3680      3690      3700      3710      3720

      3730      3740      3750      3760      3770      3780
LEX  KLSNARRHLENIMRISAILEKNCSGLDCQEQQHCEQGLSLDSHALMTYSTARISFVCPRFY
      .....
LEX  KLSNARRHLENIMRISAILEKNCSGLDCQEQQHCEQGLSLDSHALMTYSTARISFVCPRFY
      3730      3740      3750      3760      3770      3780

      3790      3800      3810      3820      3830      3840
LEX  RNVRCCTCNGGLCPGSNDPCVEKPCPGDMQCVGYEASRRPFLCQCPPGKLGECSGHTSLSF
      .....
LEX  RNVRCCTCNGGLCPGSNDPCVEKPCPGDMQCVGYEASRRPFLCQCPPGKLGECSGHTSLSF
      3790      3800      3810      3820      3830      3840

      3850      3860      3870      3880      3890      3900
LEX  AGNSYIKYRLSENSKEEDFKLALRLRTLQSNGIIMYTRANPCIILKIVDGKLWFLDCGS
      .....
LEX  AGNSYIKYRLSE
      3850
```

4589 residues in 1 query sequences

3852 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Tue Oct 21 17:24:21 2003 done: Tue Oct 21 17:24:34 2003

Scan time: 0.134 Display time: 22.466

Function used was FASTA